

## SEQUENCE LISTING

&lt;110&gt; Kenneth W. Dobie

Mark P. Roach

&lt;120&gt; ANTISENSE MODULATION OF NOD1 EXPRESSION

&lt;130&gt; RTS-0337

&lt;160&gt; 96

&lt;210&gt; 1

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Antisense Oligonucleotide

&lt;400&gt; 1

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20

&lt;210&gt; 2

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Antisense Oligonucleotide

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&lt;210&gt; 3

&lt;211&gt; 4390

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (425) ... (3286)

&lt;400&gt; 3

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gatttaaaca atgttgtttt aaaatattct aacttcaaag aatgatgcca gaaacttaaa      300
aaggggctgc gcagagtagc agggggccctg gagggcgcgg cctgaatcct gattgccctt      360
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aact atg gaa gag cag ggc cac agt gag atg gaa ata atc cca tca gag      469
      Met Glu Glu Gln Gly His Ser Glu Met Glu Ile Ile Pro Ser Glu
              1              5              10              15

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tct cac ccc cac att caa tta ctg aaa agc aat cgg gaa ctt ctg gtc      517
Ser His Pro His Ile Gln Leu Leu Lys Ser Asn Arg Glu Leu Leu Val
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act cac atc cgc aat act cag tgt ctg gtg gac aac ttg ctg aag aat      565
Thr His Ile Arg Asn Thr Gln Cys Leu Val Asp Asn Leu Leu Lys Asn
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gac tac ttc tcg gcc gaa gat gcg gag att gtg tgt gcc tgc ccc acc      613
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cag cct gac aag gtc cgc aaa att ctg gac ctg gta cag agc aag ggc      661
Gln Pro Asp Lys Val Arg Lys Ile Leu Asp Leu Val Gln Ser Lys Gly
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gag gag gtg tcc gag ttc ttc ctc tac ttg ctc cag caa ctc gca gat      709
Glu Glu Val Ser Glu Phe Phe Leu Tyr Leu Leu Gln Gln Leu Ala Asp
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gcc tac gtg gac ctc agg cct tgg ctg ctg gag atc ggc ttc tcc cct      757
Ala Tyr Val Asp Leu Arg Pro Trp Leu Leu Glu Ile Gly Phe Ser Pro
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Ser Leu Leu Thr Gln Ser Lys Val Val Val Asn Thr Asp Pro Val Ser	
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agg tat acc cag cag ctg cga cac cat ctg ggc cgt gac tcc aag ttc	853
Arg Tyr Thr Gln Gln Leu Arg His His Leu Gly Arg Asp Ser Lys Phe	
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gtg ctg tgc tat gcc cag aag gag gag ctg ctg ctg gag gag atc tac	901
Val Leu Cys Tyr Ala Gln Lys Glu Glu Leu Leu Leu Glu Glu Ile Tyr	
145 150 155	
atg gac acc atc atg gag ctg gtt ggc ttc agc aat gag agc ctg ggc	949
Met Asp Thr Ile Met Glu Leu Val Gly Phe Ser Asn Glu Ser Leu Gly	
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Ser Leu Asn Ser Leu Ala Cys Leu Leu Asp His Thr Thr Gly Ile Leu	
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Asn Glu Gln Gly Glu Thr Ile Phe Ile Leu Gly Asp Ala Gly Val Gly	
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Ser Cys Phe Lys Glu Ser Asp Arg Leu Cys Leu Gln Asp Leu Leu Phe	
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Lys His Tyr Cys Tyr Pro Glu Arg Asp Pro Glu Glu Val Phe Ala Phe	
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Leu Leu Arg Phe Pro His Val Ala Leu Phe Thr Phe Asp Gly Leu Asp	
275 280 285	

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Glu Leu His Ser Asp Leu Asp Leu Ser Arg Val Pro Asp Ser Ser Cys	
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Pro Trp Glu Pro Ala His Pro Leu Val Leu Leu Ala Asn Leu Leu Ser	
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Gly Lys Leu Leu Lys Gly Ala Ser Lys Leu Leu Thr Ala Arg Thr Gly	
320 325 330 335	
atc gag gtc ccg cgc cag ttc ctg cgg aag aag gtg ctt ctc cgg ggc	1477
Ile Glu Val Pro Arg Gln Phe Leu Arg Lys Lys Val Leu Leu Arg Gly	
340 345 350	
ttc tcc ccc agc cac ctg cgc gcc tat gcc agg agg atg ttc ccc gag	1525
Phe Ser Pro Ser His Leu Arg Ala Tyr Ala Arg Arg Met Phe Pro Glu	
355 360 365	
cgg gcc ctg cag gac cgc ctg ctg agc cag ctg gag gcc aac ccc aac	1573
Arg Ala Leu Gln Asp Arg Leu Leu Ser Gln Leu Glu Ala Asn Pro Asn	
370 375 380	
ctc tgc agc ctg tgc tct gtg ccc ctc ttc tgc tgg atc atc ttc cgg	1621
Leu Cys Ser Leu Cys Ser Val Pro Leu Phe Cys Trp Ile Ile Phe Arg	
385 390 395	
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Cys Phe Gln His Phe Arg Ala Ala Phe Glu Gly Ser Pro Gln Leu Pro	
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Asp Cys Thr Met Thr Leu Thr Asp Val Phe Leu Leu Val Thr Glu Val	
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cat ctg aac agg atg cag ccc agc agc ctg gtg cag cgg aac aca cgc	1765
His Leu Asn Arg Met Gln Pro Ser Ser Leu Val Gln Arg Asn Thr Arg	
435 440 445	
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Ser Pro Val Glu Thr Leu His Ala Gly Arg Asp Thr Leu Cys Ser Leu	
450 455 460	

ggg cag gtg gcc cac cgg ggc atg gag aag agc ctc ttt gtc ttc acc 1861  
 Gly Gln Val Ala His Arg Gly Met Glu Lys Ser Leu Phe Val Phe Thr  
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cag gag gag gtg cag gcc tcc ggg ctg cag gag aga gac atg cag ctg 1909  
 Gln Glu Glu Val Gln Ala Ser Gly Leu Gln Glu Arg Asp Met Gln Leu  
 480 485 490 495

ggc ttc ctg cgg gct ttg ccg gag ctg ggc ccc ggg ggt gac cag cag 1957  
 Gly Phe Leu Arg Ala Leu Pro Glu Leu Gly Pro Gly Gly Asp Gln Gln  
 500 505 510

tcc tat gag ttt ttc cac ctc acc ctc cag gcc ttc ttt aca gcc ttc 2005  
 Ser Tyr Glu Phe Phe His Leu Thr Leu Gln Ala Phe Phe Thr Ala Phe  
 515 520 525

ttc ctc gtg ctg gac gac agg gtg ggc act cag gag ctg ctc agg ttc 2053  
 Phe Leu Val Leu Asp Asp Arg Val Gly Thr Gln Glu Leu Leu Arg Phe  
 530 535 540

ttc cag gag tgg atg ccc cct gcg ggg gca gcg acc acg tcc tgc tat 2101  
 Phe Gln Glu Trp Met Pro Pro Ala Gly Ala Ala Thr Thr Ser Cys Tyr  
 545 550 555

cct ccc ttc ctc ccg ttc cag tgc ctg cag ggc agt ggt ccg gcg cgg 2149  
 Pro Pro Phe Leu Pro Phe Gln Cys Leu Gln Gly Ser Gly Pro Ala Arg  
 560 565 570 575

gaa gac ctc ttc aag aac aag gat cac ttc cag ttc acc aac ctc ttc 2197  
 Glu Asp Leu Phe Lys Asn Lys Asp His Phe Gln Phe Thr Asn Leu Phe  
 580 585 590

ctg tgc ggg ctg ttg tcc aaa gcc aaa cag aaa ctc ctg cgg cat ctg 2245  
 Leu Cys Gly Leu Leu Ser Lys Ala Lys Gln Lys Leu Leu Arg His Leu  
 595 600 605

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 Val Pro Ala Ala Ala Leu Arg Arg Lys Arg Lys Ala Leu Trp Ala His  
 610 615 620

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 625 630 635

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Val Glu Ser Phe Asn Gln Val Gln Ala Met Pro Thr Phe Ile Trp Met	
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Leu Arg Cys Ile Tyr Glu Thr Gln Ser Gln Lys Val Gly Gln Leu Ala	
660 665 670	
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Ala Arg Gly Ile Cys Ala Asn Tyr Leu Lys Leu Thr Tyr Cys Asn Ala	
675 680 685	
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Cys Ser Ala Asp Cys Ser Ala Leu Ser Phe Val Leu His His Phe Pro	
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Gly Gly Lys Tyr Leu Ala Leu Ala Val Lys Asn Ser Lys Ser Ile Ser	
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 865 870 875

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



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20

&lt;210&gt; 10

&lt;211&gt; 21580

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; exon:intron junction

&lt;222&gt; (15377)...(15378)

&lt;223&gt; exon 1b:intron 1b

&lt;221&gt; exon

&lt;222&gt; (18941)...(19081)

&lt;223&gt; exon 2

&lt;400&gt; 10

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&lt;213&gt; Artificial Sequence

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&lt;213&gt; Artificial Sequence

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&lt;210&gt; 96

&lt;211&gt; 1400

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; 1394

&lt;223&gt; unknown

&lt;400&gt; 96

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